

GenInfo version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 24, 2002, 01:20:41 : Search time 1474.67 seconds
(without alignments)
5403.336 Million cell updates/sec

Title: US-09-525-998a-1_copy_121_603

Perfect score: 483

Sequence: 1 gatagtggtgtgtcccccaagg.....gctacccacagattgagaat 483

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 824589755 residues

Total number of hits satisfying chosen parameters: 2944380

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- GenBank:*
- 1: gb_ba:*
- 2: gb_hgt:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vl:*
- 15: em_ba:*
- 16: em_in:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_om:*
- 20: em_or:*
- 21: em_ov:*
- 22: em_pat:*
- 23: em_ph:*
- 24: em_pl:*
- 25: em_ro:*
- 26: em_sts:*
- 27: em_sy:*
- 28: em_un:*
- 29: em_vl:*
- 30: em_hgt_hum:*
- 31: em_hgt_in:*
- 32: em_hgt_rod:*
- 33: em_hgt_hum:*
- 34: em_hgt_in:*
- 35: em_hgt_rod:*
- 36: em_hgt_other:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

Result No.	Score	Match	Length	DB	ID	Description
1	483	100.0	483	6	A29099	A29099 Synthetic D
2	483	100.0	1301	6	AF131310	AF131310 Sequence
3	483	100.0	1301	6	AF134762	AF134762 Sequence
4	483	100.0	1331	6	A29103	A29103 H.sapiens m
5	483	100.0	1368	6	A29098	A29098 Synthetic D
6	483	100.0	2050	9	HUMINRP	M60255 Human tumor
7	483	100.0	2062	6	A21523	A21522 TNF alpha g
8	483	100.0	2062	6	A29855	A29855 Sequence 24
9	483	100.0	2087	9	HUMINRP	M32244 Human tumor
10	483	100.0	2111	5	A26412	A26412 cDNA for (5
11	483	100.0	2111	9	HUMINRP	M58246 Homo sapien
12	483	100.0	2112	9	HUMINRP	M63121 Human tumor
13	483	100.0	2161	6	AK096430	AK096430 Sequence
14	483	100.0	2161	9	HUMINRP1A	X55413 H.sapiens T
15	483	100.0	2175	6	A34873	A34873 Sequence 1
16	483	100.0	2175	6	A29734	A29734 Sequence 7
17	483	100.0	2175	6	AF041076	AF041076 Sequence
18	483	100.0	2175	6	A24751	A24751 Sequence 1
19	483	100.0	2176	6	A19907	A19907 Synthetic n
20	483	100.0	2194	9	BC010143	BC010143 Homo sapi
21	483	100.0	2289	6	A26928	A26928 cDNA for 2
22	483	100.0	2289	6	AK031375	AK031375 Sequence
23	479.4	99.3	500	6	A20257	A20257 Synthetic n
24	477	98.8	513	6	A21725	A21725 cDNA for 1
25	475.2	98.4	600	6	A14806	A14806 Sequence 47
26	475	98.3	1147	6	AF131309	AF131309 Sequence
27	475	98.3	1147	6	AF134761	AF134761 Sequence
28	471	97.5	2051	6	A20255	A20255 cDNA for 1
29	424.4	87.9	1049	6	AF131307	AF131307 Sequence
30	424.4	87.9	1049	6	AF134759	AF134759 Sequence
31	424.4	87.9	1202	6	AF131308	AF131308 Sequence
32	424.4	87.9	1202	6	AF134760	AF134760 Sequence
33	383	79.3	504	6	A20713	A20713 Synthetic n
34	383	79.3	504	6	A13813	A13813 Sequence 56
35	381	78.9	501	6	A13786	A13786 Sequence 1
36	372	77.0	272	6	A20254	A20254 Synthetic n
37	372	77.0	372	6	A13787	A13787 Sequence 3
38	369	76.4	500	6	A20254	A20254 Synthetic n
39	358.2	74.2	2171	4	AF051103	AF051103 Fells cat
40	357.2	74.0	474	6	A20259	A20259 Synthetic n
41	357.2	74.0	474	6	A13809	A13809 Sequence 49
42	338.4	70.1	581	4	AF013055	AF013055 Canis fam
43	338.4	70.1	581	4	AF072344	AF072344 Fells cat
44	331.2	68.6	2004	4	SS019594	SS019594 Sus scrofa
45	331.8	68.9	2115	10	AF329976	AF329976 Rattus no

ALIGNMENTS

RESULT 1					
A29099	A29099	483 bp	DNA	PAI	04-JUL-1995
LOCUS	Synthetic cDNA for TNF-binding polyepitide from patent EP0490448.				
DEFINITION	Synthetic cDNA for TNF-binding polyepitide from patent EP0490448.				
ACCESSION	A29099				
VERSION	A29099.1	61:1248893			
KEYWORDS					
SOURCE	Synthetic construct.				
ORGANISM	Synthetic construct.				
REFERENCE	1 (bases 1 to 483)				
AUTHORS	Hauptmann, R., Hummel, A., Maurer-Erdi, I., and Stancovski, C.				
TITLE	TNF receptor, TNF-binding protein and cDNA coding therefor				
JOURNAL	Patent: EP 0490448-A 49 24 Oct 1995				
FEATURES	LOCATION/Qualifiers				
source	1..483				
	Location= "Synthetic construct"				
	/db_xref="taxon:42640"				
BASE COUNT	130 a 124 c 123 g 106 t				

ORIGIN

Query Match 100.0%; Score 483; DB 6; Length 483;
 Best Local Similarity 100.0%; Pred. No. 1,2e-139;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 qatagtgatgtcccaagaaataatatacaactcaaaaataattcgaatttgctgacc 60
 DB 1 GATAGTGTGTGTCCTCAAGAAATAATATATGACCTCAAAATAATTCGATTGTGTACC 60
 QY 61 aadtgcacaaaggaacctacttctgtaactacttccagcccgaggcgagatgacgag 120
 DB 61 AACTGCTCAATAAGCAACCTACTTCTGTAACAAATGACTGTCTCAAGCGCGGCGCAACGAGAC 120
 QY 121 taccagaaatatacaaggaagctctcaacgcttcagaaaaaacctcaagacactgctc 180
 DB 121 TGACAGCACTCTGACAGAGCGCTCTTCACTCCCTTCACAGAAACCACTCAGACACTGGCTTC 180
 QY 181 agctgtctcaaatgcagaaagaaatgggtcaggtgggaatctctctttgcacagtgag 240
 DB 181 AATTAATCAATAATGCTCAAGAAATGAGCTTAAATGAGATCTTTATGAGATGAGATGAG 240
 QY 241 cggagacacagtggtgagtgaggaagaaacccagtaacccggcatttcttgagtgaaacctt 300
 DB 241 CGGACACACCGTGTGTCGGCTTCACAGCAACCACTAGTACCGGCAATTAATGACGTGAAACACTT 300
 QY 301 tttccagtgtlccaatltcagacgtctcctccataggaacatgcacclctcctcagcagag 360
 DB 301 TTCCAGTGTCTCAATGTGACACCTCTGCCCTCAATGCGACCTTCCTGCGCAGAG 360
 QY 361 aaacaaacacagtgctgacgtcgcctgacagtgcttctctttaaagaaacagagtgctc 420
 DB 361 AAACAGACACGCTCTGAAATGATATGATATGATATGATATGATATGATATGATATGATATGAT 420
 QY 421 tctctaatatgctgaagaaagcgtgagtgagtgagtgagtgagtgagtgagtgagtgag 480
 DB 421 TCTCTAATATGCTGAAGAAAGCCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 480
 QY 481 aat 483
 DB 481 AAT 483

RESULT 2

AR131410
 LOCUS AR131410 1301 bp DNA PAT 16-MAY-2001
 DEFINITION Sequence 7 from patent US 6193972.
 ACCESSION AR131410
 VERSION AR131410.1 GI:14120213
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1301)
 AUTHORS Campbell, P. K., Jameson, R. A. and Chappell, S. C.
 TITLE Hybrid heterodimeric protein hormone
 JOURNAL Patent: US 6193972-A 7 27-FEB-2001;
 FEATURES Location/Qualifiers
 Source 1..1301
 BASE COUNT 269 a 413 c 351 g 268 t
 ORIGIN

Query Match 100.0%; Score 483; DB 6; Length 1301;
 Best Local Similarity 100.0%; Pred. No. 1,2e-139;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 qatagtgatgtcccaagaaataatatacaactcaaaaataattcgaatttgctgacc 60
 DB 345 GATAGTGTGTGTCCTCAAGAAATAATATGACCTCAAAATAATTCGATTGTGTACC 404

QY 61 aadtgcacaaaggaacctacttctgtaactacttccagcccgaggcgagatgacgag 120
 DB 465 AATTAATCAATAAGCAACCTACTTCTGTAACAAATGACTGTCTCAAGCGCGGCGCAACGAGAC 464
 QY 121 taccagaaatatacaaggaagctctcaacgcttcagaaaaaacctcaagacactgctc 180
 DB 465 TGACAGCACTCTGACAGAGCGCTCTTCACTCCCTTCACAGAAACCACTCAGACACTGGCTTC 524
 QY 181 aactgcacaaaggaacctacttctgtaactacttccagcccgaggcgagatgacgag 240
 DB 525 AATTAATCAATAAGCAACCTACTTCTGTAACAAATGACTGTCTCAAGCGCGGCGCAACGAGAC 584
 QY 241 cggagacacagtggtgagtgaggaagaaacccagtaacccggcatttcttgagtgaaacctt 300
 DB 585 CGGACACACCGTGTGTCGGCTTCACAGCAACCACTAGTACCGGCAATTAATGAGTGAAGTGAAG 644
 QY 301 tttccagtgtlccaatltcagacgtctcctccataggaacatgcacclctcctcagcagag 360
 DB 645 TTCCAGTGTCTCAATGTGACACCTTCGCCCTCAATGCGACCTTCCTGCGCAGAG 704
 QY 361 aaacaaacacagtgctgacgtcgcctgacagtgcttctctttaaagaaacagagtgctc 420
 DB 705 AAACAGACACGCTCTGAAATGATATGATATGATATGATATGATATGATATGATATGATATGAT 764
 QY 421 tctctaatatgctgaagaaagcgtgagtgagtgagtgagtgagtgagtgagtgagtgag 480
 DB 765 TCTCTAATATGCTGAAGAAAGCCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 824
 QY 481 aat 483
 DB 825 AAT 827

RESULT 3

AR134762
 LOCUS AR134762 1301 bp DNA PAT 16 MAY 2001
 DEFINITION Sequence 7 from patent US 6194177.
 ACCESSION AR134762
 VERSION AR134762.1 GI:14123667
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1301)
 AUTHORS Campbell, P. K., Jameson, R. A. and Chappell, S. C.
 TITLE DNA encoding a hybrid heterodimeric protein
 JOURNAL Patent: US 6194177-A 7 27-FEB-2001;
 FEATURES Location/Qualifiers
 Source 1..1301
 BASE COUNT 269 a 413 c 351 g 268 t
 ORIGIN

Query Match 100.0%; Score 483; DB 6; Length 1301;
 Best Local Similarity 100.0%; Pred. No. 1,2e-139;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 qatagtgatgtcccaagaaataatatacaactcaaaaataattcgaatttgctgacc 60
 DB 345 GATAGTGTGTGTCCTCAAGAAATAATATGACCTCAAAATAATTCGATTGTGTACC 404
 QY 61 aadtgcacaaaggaacctacttctgtaactacttccagcccgaggcgagatgacgag 120
 DB 405 AATTAATCAATAAGCAACCTACTTCTGTAACAAATGACTGTCTCAAGCGCGGCGCAACGAGAC 464
 QY 121 taccagaaatatacaaggaagctctcaacgcttcagaaaaaacctcaagacactgctc 180
 DB 465 TGACAGCACTCTGACAGAGCGCTCTTCACTCCCTTCACAGAAACCACTCAGACACTGGCTTC 524
 QY 181 aactgcacaaaggaacctacttctgtaactacttccagcccgaggcgagatgacgag 240
 DB 525 AATTAATCAATAAGCAACCTACTTCTGTAACAAATGACTGTCTCAAGCGCGGCGCAACGAGAC 584

SKTKEMQAVETISCTVDPTQVQPKNOYRHYWSENLEPCFNCSLGNGTSHLSQCE
KONTVCTHAGFTLRENEVQSCNKKSLKTLKLPQTFNVKGTGDSCTTVILPLVI
PFGCLLSLILFGLMYRQPKSKLYIVCGKSTPKKELEGKTKPLAPNPSPT
PGFTPIILGFSVAPSSSTHLSSTVTPGDCNPAAPREVAAPPYOGADPILALASDPI
PNPLQKKEADSHKPSQSLDSDPATLYAVVENVPPLRWKEFVRRGLSDHLELQON
GRCLREAYQSMLATWRPPTPPREATLEILGVLPLMDLLGLCLEDIEEALGCPAALPPA
PSLLR"

gene 187..1554
/gene="TNF receptor"
mat_peptide 274..1551
/gene="TNF receptor"
/product="tumor necrosis factor receptor"
BASE COUNT 445 a 629 c 587 g 450 t
ORIGIN

Query Match 100.0%; Score 483; DB 9; Length 2111;
Best Local Similarity 100.0%; Pred. No. 120-130;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 gatagtgtgtgtccccaaggaataatataccacccctcaaatatattogatttctgtacc 60
Db 307 GATAGTGTGTGTCGCCCAAGCAAAATATATCCACCTTCAAAATAATTCGATTTCCTGTACC 366
Oy 61 aagtgcacaagaacacclactlglacaatgaclgtccaggcccgaggaagacagac 120
Db 367 AAGTGTGTGTCGCCCAAGCAAAATATATCCACCTTCAAAATAATTCGATTTCCTGTACC 426
Oy 121 tgcaggaggtgtgagagcggctctcttaccagcttcaaaaacacacacacacacac 180
Db 427 TGCAGGAGGTGTGAG 486
Oy 181 agctactccaaatgccgaagaagaatgggtcaggtgagatctcttcttgcacagtgag 240
Db 487 AGCTGTGTGTGTCGCCCAAGCAAAATATATCCACCTTCAAAATAATTCGATTTCCTGTACC 546
Oy 241 caggaacacaggtgtgag 300
Db 547 CCGGACACCGTGTGTCGCCCAAGCAAAATATATCCACCTTCAAAATAATTCGATTTCCTGTACC 606
Oy 301 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 360
Db 607 TTCTGTGTGTGTCGCCCAAGCAAAATATATCCACCTTCAAAATAATTCGATTTCCTGTACC 666
Oy 361 aaacagacacagctgtgcacctgcacagagagagagagagagagagagagagagagagag 420
Db 667 AAACAGACACCGTGTGTCGCCCAAGCAAAATATATCCACCTTCAAAATAATTCGATTTCCTGTACC 726
Oy 421 tccctgaatgaactatgaagaagcctgaatgcacagaggttgcacacacacacagagagag 480
Db 727 TCCGTGTGTGTGTCGCCCAAGCAAAATATATCCACCTTCAAAATAATTCGATTTCCTGTACC 786
Oy 481 aat 483
Db 787 AAT 789

RESULT 12
LOCUS HUMTNFR 2112 bp mRNA PRI 03-AUG 1993
DEFINITION Human tumor necrosis factor receptor (TNF receptor) mRNA, complete cds.
ACCESSION M63121 M75861
VERSION M63121.1 GI:339755
KEYWORDS tumor necrosis factor receptor.
SOURCE human cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.
REFERENCE
1 (bases 1 to 2112)
Himmler, A., Maurer-Fogy, I., Kroenke, M., Scheurich, P.,
Pflizmaier, K., Lantiz, M., Olsson, I., Haupmann, P., Stratowa, C. and
Adolf, G.R.

TITLE Molecular cloning and expression of human and rat tumor necrosis
factor receptor chain (p40) and its soluble derivative, tumor
necrosis factor-binding protein
JOURNAL DNA Cell Biol. 9, 705-715 (1990)
MEDLINE 91090841
FEATURES
source
.. 2112
/organism="Homo sapiens"
/db_xref="taxon:9606"
sig_peptide 207..293
CDS
207..1574
/gene="TNF receptor"
/codon_start=1
/product="tumor necrosis factor receptor"
/protein_id="AAA46754.1"
/db_xref="GI:339755"

gene 207..1574
/gene="TNF receptor"
mat_peptide 294..1571
/gene="TNF receptor"
/product="tumor necrosis factor receptor"
BASE COUNT 435 a 632 c 589 g 456 t
ORIGIN

Query Match 100.0%; Score 483; DB 9; Length 2112;
Best Local Similarity 100.0%; Pred. No. 120-139;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 gatagtgtgtgtccccaaggaataatataccacccctcaaatatattogatttctgtacc 60
Db 327 GATAGTGTGTGTCGCCCAAGCAAAATATATCCACCTTCAAAATAATTCGATTTCGTAAC 386
Oy 61 aagtgcacaagaacacclactlglacaatgaclgtccaggcccgaggaagacagac 120
Db 387 AAGTGTGTGTCGCCCAAGCAAAATATATCCACCTTCAAAATAATTCGATTTCGTAAC 446
Oy 121 tgcaggaggtgtgagagcggctctcttaccagcttcaaaaacacacacacacacac 180
Db 447 TGCAGGAGGTGTGAG 506
Oy 181 agctactccaaatgccgaagaagaatgggtcaggtgagatctcttcttgcacagtgag 240
Db 507 AGCTGTGTGTGTCGCCCAAGCAAAATATATCCACCTTCAAAATAATTCGATTTCGTAAC 566
Oy 241 caggaacacaggtgtgcacctgcacagagagagagagagagagagagagagagagagag 300
Db 567 CCGGACACCGTGTGTCGCCCAAGCAAAATATATCCACCTTCAAAATAATTCGATTTCGTAAC 626
Oy 301 ttccagtgcttcaattgcagcctctgcctcaatgggaccgtgcacctctcctgccaggag 360
Db 627 TCCGTGTGTGTGTCGCCCAAGCAAAATATATCCACCTTCAAAATAATTCGATTTCGTAAC 686
Oy 361 aaacagacacagctgtgcacctgcacagagagagagagagagagagagagagagagagag 420
Db 687 AAACAGACACCGTGTGTCGCCCAAGCAAAATATATCCACCTTCAAAATAATTCGATTTCGTAAC 746
Oy 421 tccctgaatgaactatgaagaagcctgaatgcacagaggttgcacacacacagagagag 480
Db 747 TCCGTGTGTGTGTCGCCCAAGCAAAATATATCCACCTTCAAAATAATTCGATTTCGTAAC 806
Oy 481 aat 483
Db 807 AAT 809

